

# SCORE Search Results Details for Application 10010742 and Search Result 20070109\_163058\_us-10-010-742-52.rng.

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 02:40:48 ; Search time 418 Seconds  
(without alignments)  
6321.728 Million cell updates/sec

Title: US-10-010-742-52

Perfect score: 379

Sequence: 1 actttgccaaggcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
1	379	100.0	379	4	AAH55527	Aah55527 Human bre
2	379	100.0	379	7	ADU01271	Adu01271 Breast ca
3	379	100.0	379	7	ADZ41535	Adz41535 Human bre
4	379	100.0	379	12	ADN40297	Adn40297 Human bre
c 5	379	100.0	397	4	AAL13663	Aal13663 Human bre
c 6	379	100.0	403	4	AAL18673	Aal18673 Human bre
c 7	379	100.0	598	5	ABV24442	Abv24442 Human pro
c 8	379	100.0	598	5	ABV28048	Abv28048 Human pro
c 9	379	100.0	870	11	ACN83733	Acn83733 Breast ca
c 10	379	100.0	963	7	ADU01522	Adu01522 Breast ca
c 11	379	100.0	963	7	ADZ41786	Adz41786 Human bre
c 12	379	100.0	1299	11	ACN89634	Acn89634 Breast ca
c 13	379	100.0	1518	7	ADU01524	Adu01524 Breast ca
c 14	379	100.0	1518	7	ADZ41788	Adz41788 Human bre
c 15	379	100.0	1518	12	ADQ48399	Adq48399 Human cyt
c 16	379	100.0	1586	4	AAD09946	Aad09946 Human dru
c 17	379	100.0	1598	7	ADU01521	Adu01521 Breast ca
c 18	379	100.0	1598	7	ADZ41785	Adz41785 Human bre
c 19	379	100.0	1743	12	ADJ67057	Adj67057 Human sec
c 20	379	100.0	1894	6	ABT07693	Abt07693 Breast ca
c 21	379	100.0	1906	12	ADQ36612	Adq36612 Human CYP
c 22	379	100.0	1975	10	AAD60551	Aad60551 Human cyt
c 23	379	100.0	1975	10	ACA61906	Aca61906 cDNA enco
c 24	379	100.0	1975	12	ADQ48397	Adq48397 Human cyt
c 25	379	100.0	2015	6	AAD24015	Aad24015 Human dru
c 26	379	100.0	2015	7	ADU01523	Adu01523 Breast ca
c 27	379	100.0	2015	7	ADZ41787	Adz41787 Human bre
c 28	379	100.0	2020	6	ABK33550	Abk33550 cDNA enco
c 29	379	100.0	2020	7	ADY31769	Ady31769 Novel hum
c 30	379	100.0	2020	8	ACA68511	Aca68511 Novel hum
c 31	379	100.0	2020	9	ABT44240	Abt44240 Human PRO
c 32	379	100.0	2020	9	ABT44523	Abt44523 Human PRO
c 33	379	100.0	2020	9	ACD82190	Acd82190 Human sec
c 34	379	100.0	2020	9	ABT43896	Abt43896 Human mem
c 35	379	100.0	2020	9	ADB83519	Adb83519 Novel hum
c 36	379	100.0	2020	9	ADB80625	Adb80625 Novel hum
c 37	379	100.0	2020	9	ADB73166	Adb73166 Novel hum
c 38	379	100.0	2020	9	ADB78248	Adb78248 Novel hum
c 39	379	100.0	2020	10	ADB84896	Adb84896 Human PRO
c 40	379	100.0	2020	10	ADB78002	Adb78002 Novel hum
c 41	379	100.0	2020	10	ADB87068	Adb87068 Human PRO
c 42	379	100.0	2020	10	ADB84650	Adb84650 Human PRO
c 43	379	100.0	2020	10	ADB83765	Adb83765 Novel hum
c 44	379	100.0	2020	10	ADB72920	Adb72920 Novel hum
c 45	379	100.0	2020	10	ADC36758	Adc36758 Human PRO

## ALIGNMENTS

RESULT 1

# SCORE Search Results Details for Application 10010742 and Search Result \$itemName.

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 02:47:13 ; Search time 2707 Seconds  
(without alignments)  
8953.111 Million cell updates/sec

Title: US-10-010-742-52  
Perfect score: 379  
Sequence: 1 actttgccaaggcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_env:\*

2: gb\_pat:\*

3: gb\_ph:\*

4: gb\_pl:\*

5: gb\_pr:\*

6: gb\_ro:\*

7: gb\_sts:\*

8: gb\_sy:\*

9: gb\_un:\*

10: gb\_vi:\*

11: gb\_ov:\*

12: gb\_htg:\*

13: gb\_in:\*

14: gb\_om:\*

15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					%	Description
No.	Score	Match	Length	DB	ID		
1	379	100.0	379	2	CS110385		CS110385 Sequence
2	379	100.0	379	2	AX156195		AX156195 Sequence
c 3	379	100.0	397	2	CQ421094		CQ421094 Sequence
4	379	100.0	403	2	CQ426106		CQ426106 Sequence
c 5	379	100.0	598	2	CQ492564		CQ492564 Sequence
c 6	379	100.0	598	2	CQ496194		CQ496194 Sequence
c 7	379	100.0	963	2	CS110636		CS110636 Sequence
c 8	379	100.0	1518	2	CS110638		CS110638 Sequence
c 9	379	100.0	1548	2	CS110645		CS110645 Sequence
c 10	379	100.0	1586	2	AX195182		AX195182 Sequence
c 11	379	100.0	1598	2	CS110635		CS110635 Sequence
c 12	379	100.0	1894	2	AX829108		AX829108 Sequence
c 13	379	100.0	1907	5	AY262056		AY262056 Homo sapi
c 14	379	100.0	2015	2	CS110637		CS110637 Sequence
c 15	379	100.0	2015	2	AX317983		AX317983 Sequence
c 16	379	100.0	2020	2	CQ970464		CQ970464 Sequence
c 17	379	100.0	2020	2	AX358776		AX358776 Sequence
c 18	379	100.0	2020	2	AX362269		AX362269 Sequence
c 19	379	100.0	2020	5	AY358631		AY358631 Homo sapi
c 20	377.4	99.6	386	2	CQ430462		CQ430462 Sequence
c 21	377.4	99.6	393	2	CQ418480		CQ418480 Sequence
c 22	377.4	99.6	393	2	CQ421061		CQ421061 Sequence
c 23	377.4	99.6	393	2	CQ426250		CQ426250 Sequence
c 24	372	98.2	651	2	CQ421181		CQ421181 Sequence
c 25	369.4	97.5	792	2	CQ430054		CQ430054 Sequence
c 26	367	96.8	392	2	CQ429968		CQ429968 Sequence
c 27	365.4	96.4	392	2	CQ429935		CQ429935 Sequence
28	365.4	96.4	397	2	CQ421574		CQ421574 Sequence
29	363	95.8	393	2	CQ430100		CQ430100 Sequence
30	363	95.8	415	2	CQ421229		CQ421229 Sequence
c 31	363	95.8	1436	5	AY262057		AY262057 Homo sapi
c 32	363	95.8	2608	2	CS168612		CS168612 Sequence
c 33	363	95.8	2608	2	AX834733		AX834733 Sequence
c 34	363	95.8	2608	5	AK097373		AK097373 Homo sapi
c 35	361.4	95.4	392	2	CQ426196		CQ426196 Sequence
c 36	357.2	94.2	1503	2	AX768910		AX768910 Sequence
37	356	93.9	422	2	CQ418336		CQ418336 Sequence
c 38	342.4	90.3	357	2	CQ421595		CQ421595 Sequence
c 39	329.4	86.9	364	2	CQ426051		CQ426051 Sequence
c 40	317.6	83.8	391	2	CQ417373		CQ417373 Sequence
c 41	313.8	82.8	396	2	CQ418426		CQ418426 Sequence
42	312.4	82.4	318	2	CQ430441		CQ430441 Sequence
c 43	253.6	66.9	1197	5	AY696295		AY696295 Homo sapi
44	235.2	62.1	444	2	CQ505007		CQ505007 Sequence
45	235.2	62.1	444	2	CQ510749		CQ510749 Sequence

## ALIGNMENTS

RESULT 1

CS110385

LOCUS CS110385

379 bp DNA linear PAT 22-JUN-2005

# SCORE Search Results Details for Application 10010742 and Search Result 20070109\_163104\_us-10-010-742-52.rst.

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 02:54:23 ; Search time 3144 Seconds  
(without alignments)  
6740.912 Million cell updates/sec

Title: US-10-010-742-52  
Perfect score: 379  
Sequence: 1 actttgccaaggcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est3:\*

3: gb\_est4:\*

4: gb\_est5:\*

5: gb\_est6:\*

6: gb\_htc:\*

7: gb\_est2:\*

8: gb\_est7:\*

9: gb\_est8:\*

10: gb\_est9:\*

11: gb\_gss1:\*

12: gb\_gss2:\*

13: gb\_gss3:\*

14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

%

Result	Query					Description
No.	Score	Match	Length	DB	ID	
c 1	154.6	40.8	770	2	BI913122	BI913122 603179852
c 2	154.6	40.8	1335	14	AY408468	AY408468 Homo sapi
c 3	149.2	39.4	559	9	DA362614	DA362614 DA362614
c 4	141	37.2	623	1	AA193450	AA193450 zr40e07.r
c 5	140.4	37.0	1329	14	AY408470	AY408470 Mus muscu
c 6	140.4	37.0	3860	6	AK038526	AK038526 Mus muscu
c 7	128.6	33.9	628	4	BX272921	BX272921 BX272921
c 8	128.6	33.9	651	4	BX267843	BX267843 BX267843
c 9	128.6	33.9	676	5	CD216415	CD216415 pgp2n.pk0
c 10	125.6	33.1	786	5	CF547569	CF547569 AGENCOURT
c 11	124	32.7	869	10	DR860522	DR860522 JGI_CABG5
c 12	124	32.7	874	9	CX967511	CX967511 JGI_CAAP2
c 13	124	32.7	1642	6	BC054308	BC054308 Xenopus l
c 14	121	31.9	567	7	BF509149	BF509149 UI-H-BI4-
c 15	119.8	31.6	218	11	AY758967	AY758967 CH255-13m
c 16	119.8	31.6	556	5	CD734809	CD734809 4048891 1
c 17	119.2	31.5	735	3	BU243372	BU243372 603778833
c 18	118.2	31.2	839	3	BU227845	BU227845 603947881
c 19	116.6	30.8	824	9	CX966129	CX966129 JGI_CAAP1
c 20	116	30.6	792	2	BG193485	BG193485 RST12619
c 21	115.2	30.4	767	5	CJ023895	CJ023895 CJ023895
c 22	115	30.3	655	2	BJ909012	BJ909012 BJ909012
c 23	114.4	30.2	817	10	DR860523	DR860523 JGI_CABG5
c 24	114	30.1	773	2	BG461834	BG461834 RST44771
c 25	112	29.6	740	3	BP435575	BP435575 BP435575
c 26	112	29.6	813	3	BP435822	BP435822 BP435822
c 27	112	29.6	841	5	CJ025855	CJ025855 CJ025855
c 28	112	29.6	870	5	CJ022965	CJ022965 CJ022965
c 29	112	29.6	932	3	BQ881161	BQ881161 AGENCOURT
c 30	111.4	29.4	769	4	CA487879	CA487879 AGENCOURT
c 31	111.4	29.4	1038	2	BG291597	BG291597 602388704
c 32	111.2	29.3	252	2	BG204180	BG204180 RST23576
c 33	110.4	29.1	808	5	CJ022616	CJ022616 CJ022616
c 34	109.6	28.9	741	4	CB599980	CB599980 AGENCOURT
c 35	109.6	28.9	759	4	CB950823	CB950823 AGENCOURT
c 36	109.6	28.9	779	4	CB600740	CB600740 AGENCOURT
c 37	108.8	28.7	735	5	CK471537	CK471537 AGENCOURT
c 38	108.8	28.7	746	5	CK364271	CK364271 AGENCOURT
c 39	108.8	28.7	805	10	DR428109	DR428109 naw50f07.
c 40	108.8	28.7	864	8	CO554538	CO554538 AGENCOURT
c 41	108	28.5	570	4	CB601086	CB601086 AGENCOURT
c 42	108	28.5	622	2	BG971712	BG971712 602838239
c 43	108	28.5	640	2	BG971106	BG971106 602837813
c 44	108	28.5	651	7	BE851329	BE851329 uw94g07.y
c 45	108	28.5	747	4	CB953130	CB953130 AGENCOURT

## ALIGNMENTS

RESULT 1  
BI913122/c

# SCORE Search Results Details for Application 10010742 and Search Result 20070109\_163108\_us-10-010-742-52.rni.

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 03:39:33 ; Search time 144 Seconds  
(without alignments)  
4924.654 Million cell updates/sec

Title: US-10-010-742-52

Perfect score: 379

Sequence: 1 actttgc当地aaagg.....ttcaggtatgagtc当地agggt 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
c	1	154.6	40.8	1508	3	US-09-799-451-109	Sequence 109, App
c	2	154.6	40.8	2071	3	US-10-104-047-720	Sequence 720, App
c	3	154.6	40.8	2327	3	US-09-852-067-1	Sequence 1, Appli
c	4	154.6	40.8	2327	3	US-10-338-691-1	Sequence 1, Appli
c	5	153	40.4	1718	3	US-09-799-451-420	Sequence 420, App
c	6	111.4	29.4	2084	3	US-09-023-655-1045	Sequence 1045, Ap
c	7	98.4	26.0	2382	3	US-09-023-655-1436	Sequence 1436, Ap
c	8	96.8	25.5	2576	4	US-09-880-107-2138	Sequence 2138, Ap
c	9	82.6	21.8	1763	4	US-09-880-107-1610	Sequence 1610, Ap
c	10	73.4	19.4	300	3	US-09-172-108-2	Sequence 2, Appli
c	11	73.4	19.4	300	3	US-09-172-711-3	Sequence 3, Appli
c	12	69.8	18.4	1634	5	US-10-114-270-59	Sequence 59, Appl
c	13	69.8	18.4	1669	3	US-09-976-594-532	Sequence 532, App
c	14	66.6	17.6	2227	3	US-09-023-655-1433	Sequence 1433, Ap
c	15	66.4	17.5	888	3	US-09-023-655-198	Sequence 198, App
c	16	66.4	17.5	1676	3	US-09-991-181-263	Sequence 263, App
c	17	66.4	17.5	1676	3	US-09-990-444-263	Sequence 263, App
c	18	66.4	17.5	1676	3	US-09-997-333-263	Sequence 263, App
c	19	66.4	17.5	1676	3	US-09-992-598-263	Sequence 263, App
c	20	66.4	17.5	1676	4	US-09-989-735-263	Sequence 263, App
c	21	66.4	17.5	1676	5	US-09-989-726-263	Sequence 263, App
c	22	66.4	17.5	1676	5	US-09-997-514-263	Sequence 263, App
c	23	66.4	17.5	1676	5	US-09-989-728-263	Sequence 263, App
c	24	66.4	17.5	1676	5	US-09-997-349-263	Sequence 263, App
c	25	66.4	17.5	1676	5	US-09-997-653-263	Sequence 263, App
c	26	66.4	17.5	1676	5	US-09-989-293A-263	Sequence 263, App
c	27	66.4	17.5	2412	3	US-10-104-047-824	Sequence 263, App
c	28	65	17.2	2073	3	US-09-023-655-1385	Sequence 824, App
c	29	65	17.2	2073	4	US-09-880-107-1601	Sequence 1385, Ap
c	30	65	17.2	2369	4	US-09-880-107-3277	Sequence 1601, Ap
c	31	65	17.2	5050	3	US-09-949-016-132	Sequence 3277, Ap
c	32	64.4	17.0	31208	3	US-09-852-067-3	Sequence 132, App
c	33	64.4	17.0	31208	3	US-10-338-691-3	Sequence 3, Appli
c	34	64.2	16.9	1185	3	US-09-023-655-1270	Sequence 3, Appli
c	35	64.2	16.9	2367	3	US-09-949-016-4207	Sequence 1270, Ap
36	55.2	14.6	285	3	US-09-020-956-153	Sequence 4207, Ap	
37	55.2	14.6	285	3	US-09-030-607-153	Sequence 153, App	
38	55.2	14.6	285	3	US-09-439-313-153	Sequence 153, App	
39	55.2	14.6	285	3	US-09-352-616A-153	Sequence 153, App	
40	55.2	14.6	285	3	US-09-232-149A-153	Sequence 153, App	
41	55.2	14.6	285	3	US-09-159-812-153	Sequence 153, App	
42	55.2	14.6	285	3	US-09-636-215-153	Sequence 153, App	
43	55.2	14.6	285	3	US-09-685-166A-153	Sequence 153, App	
44	55.2	14.6	285	3	US-09-115-453-153	Sequence 153, App	
45	55.2	14.6	285	3	US-09-688-489-153	Sequence 153, App	

## ALIGNMENTS

## RESULT 1

US-09-799-451-109/c  
; Sequence 109, Application US/09799451  
; Patent No. 6783969  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom

# SCORE Search Results Details for Application 10010742 and Search Result 20070109\_163111\_us-10-010-742-52.rnpbm.

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OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 04:32:09 ; Search time 924 Seconds  
(without alignments)  
5040.058 Million cell updates/sec

Title: US-10-010-742-52

Perfect score: 379

Sequence: 1 actttgccaaggcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_NA\_Main:\*

```

1: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US08_PUBCOMB.seq:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
10: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
15: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11C_PUBCOMB.seq:*
```

16: /EMC\_Celerra\_SIDS3/ptodata/2/pubpna/US11D\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	379	100.0	379	3	US-09-778-320-52	Sequence 52, Appl
2	379	100.0	379	3	US-09-910-689-52	Sequence 52, Appl
3	379	100.0	379	6	US-10-010-742-52	Sequence 52, Appl
4	379	100.0	379	8	US-10-714-389-52	Sequence 52, Appl
5	379	100.0	379	8	US-10-717-296-52	Sequence 52, Appl
c 6	379	100.0	598	9	US-10-357-930-24431	Sequence 24431, A
c 7	379	100.0	598	9	US-10-357-930-28061	Sequence 28061, A
c 8	379	100.0	870	6	US-10-198-846-4883	Sequence 4883, Ap
c 9	379	100.0	963	3	US-09-910-689-303	Sequence 303, App
c 10	379	100.0	963	6	US-10-010-742-303	Sequence 303, App
c 11	379	100.0	963	8	US-10-717-296-303	Sequence 303, App
c 12	379	100.0	1299	6	US-10-198-846-10784	Sequence 10784, A
c 13	379	100.0	1518	3	US-09-910-689-305	Sequence 305, App
c 14	379	100.0	1518	6	US-10-010-742-305	Sequence 305, App
c 15	379	100.0	1518	6	US-10-067-668-3	Sequence 3, Appli
c 16	379	100.0	1518	6	US-10-175-696-3	Sequence 3, Appli
c 17	379	100.0	1518	8	US-10-776-871-3	Sequence 3, Appli
c 18	379	100.0	1518	8	US-10-717-296-305	Sequence 305, App
c 19	379	100.0	1548	8	US-10-717-296-312	Sequence 312, App
c 20	379	100.0	1586	8	US-10-181-108-35	Sequence 35, Appli
c 21	379	100.0	1586	13	US-11-079-743-35	Sequence 35, Appli
c 22	379	100.0	1598	3	US-09-910-689-302	Sequence 302, App
c 23	379	100.0	1598	6	US-10-010-742-302	Sequence 302, App
c 24	379	100.0	1598	8	US-10-717-296-302	Sequence 302, App
c 25	379	100.0	1894	8	US-10-058-270A-1	Sequence 1, Appli
c 26	379	100.0	1975	6	US-10-067-668-1	Sequence 1, Appli
c 27	379	100.0	1975	6	US-10-175-696-1	Sequence 1, Appli
c 28	379	100.0	1975	8	US-10-776-871-1	Sequence 1, Appli
c 29	379	100.0	2015	3	US-09-910-689-304	Sequence 304, App
c 30	379	100.0	2015	6	US-10-010-742-304	Sequence 304, App
c 31	379	100.0	2015	8	US-10-296-606-23	Sequence 23, Appli
c 32	379	100.0	2015	8	US-10-717-296-304	Sequence 304, App
c 33	379	100.0	2020	6	US-10-227-884-29	Sequence 29, Appli
c 34	379	100.0	2020	6	US-10-230-163-29	Sequence 29, Appli
c 35	379	100.0	2020	6	US-10-230-338-29	Sequence 29, Appli
c 36	379	100.0	2020	6	US-10-218-631-29	Sequence 29, Appli
c 37	379	100.0	2020	6	US-10-230-414-29	Sequence 29, Appli
c 38	379	100.0	2020	6	US-10-232-224-29	Sequence 29, Appli
c 39	379	100.0	2020	6	US-10-216-159A-29	Sequence 29, Appli
c 40	379	100.0	2020	6	US-10-218-849-29	Sequence 29, Appli
c 41	379	100.0	2020	6	US-10-227-873-29	Sequence 29, Appli
c 42	379	100.0	2020	6	US-10-227-883-29	Sequence 29, Appli
c 43	379	100.0	2020	6	US-10-219-076-29	Sequence 29, Appli
c 44	379	100.0	2020	6	US-10-230-434-29	Sequence 29, Appli
c 45	379	100.0	2020	6	US-10-219-003-29	Sequence 29, Appli

## ALIGNMENTS

# SCORE Search Results Details for Application 10010742 and Search Result 20070109\_163115\_us-10-010-742-52.rnpbn.

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Suggestions](#)

This page gives you Search Results detail for the Application 10010742 and Search Result 20070109\_163115\_us-10-010-742-52.rnpbn.

[start](#) | [next page](#)

[Go Back to previous page](#)

GenCore version 5.1.9  
Copyright (c) 1993 - 2007 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 11, 2007, 04:34:33 ; Search time 726 Seconds  
(without alignments)  
1422.648 Million cell updates/sec

Title: US-10-010-742-52

Perfect score: 379

Sequence: 1 actttgccaaggcagtaaagg.....ttcaggtatgagtccagggt 379

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3650718 seqs, 1362588608 residues

Total number of hits satisfying chosen parameters: 7301436

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_NA\_New:\*

1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq1:\*

9: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*

10: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*

11: /EMC\_Celerra\_SIDS3/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
c 1	379	100.0	1906	6	US-10-540-310-3	Sequence 3, Appli
c 2	363	95.8	2608	8	US-11-293-697-1857	Sequence 1857, Ap
c 3	154.6	40.8	1555	8	US-11-266-748A-367721	Sequence 367721,
c 4	154.6	40.8	1555	8	US-11-266-748A-451100	Sequence 451100,
c 5	154.6	40.8	2343	6	US-10-131-833A-107	Sequence 107, App
c 6	154.6	40.8	2349	8	US-11-293-697-2301	Sequence 2301, Ap
c 7	154.6	40.8	2382	8	US-11-266-748A-56478	Sequence 56478, A
c 8	154	40.6	1000	8	US-11-266-748A-203310	Sequence 203310,
c 9	154	40.6	1000	8	US-11-266-748A-283212	Sequence 283212,
c 10	154	40.6	1000	8	US-11-266-748A-309852	Sequence 309852,
c 11	154	40.6	1000	8	US-11-266-748A-392920	Sequence 392920,
c 12	154	40.6	1000	8	US-11-266-748A-483638	Sequence 483638,
c 13	154	40.6	193471	8	US-11-266-748A-23901	Sequence 23901, A
c 14	114.4	30.2	2376	8	US-11-293-697-2332	Sequence 2332, Ap
c 15	111.4	29.4	1539	7	US-11-371-354-5351	Sequence 5351, Ap
c 16	111.4	29.4	1539	7	US-11-371-354-60240	Sequence 60240, A
c 17	111.4	29.4	1558	8	US-11-266-748A-78471	Sequence 78471, A
c 18	111.4	29.4	1558	8	US-11-266-748A-131282	Sequence 131282,
c 19	111.4	29.4	2147	10	US-11-090-997-1025	Sequence 1025, Ap
c 20	108	28.5	1871	10	US-11-090-997-135	Sequence 135, App
c 21	108	28.5	1871	10	US-11-397-327-38	Sequence 38, Appl
c 22	100.4	26.5	1754	8	US-11-266-748A-361338	Sequence 361338,
c 23	100.4	26.5	1754	8	US-11-266-748A-444717	Sequence 444717,
c 24	98.4	26.0	1000	8	US-11-266-748A-394439	Sequence 394439,
c 25	98.4	26.0	1000	8	US-11-266-748A-465485	Sequence 465485,
c 26	96.8	25.5	1368	7	US-11-371-354-6869	Sequence 6869, Ap
c 27	96.8	25.5	1368	7	US-11-371-354-64400	Sequence 64400, A
c 28	95.2	25.1	779	8	US-11-266-748A-262386	Sequence 262386,
c 29	95.2	25.1	779	8	US-11-266-748A-322903	Sequence 322903,
c 30	94	24.8	877	8	US-11-266-748A-214290	Sequence 214290,
c 31	93	24.5	1000	8	US-11-266-748A-293498	Sequence 293498,
c 32	93	24.5	1000	8	US-11-266-748A-344927	Sequence 344927,
c 33	89	23.5	600	8	US-11-266-748A-102267	Sequence 102267,
c 34	89	23.5	600	8	US-11-266-748A-155078	Sequence 155078,
c 35	79.8	21.1	947	8	US-11-266-748A-186910	Sequence 186910,
c 36	79.8	21.1	947	8	US-11-266-748A-241605	Sequence 241605,
c 37	75	19.8	2608	8	US-11-293-697-1514	Sequence 1514, Ap
c 38	69.8	18.4	1575	7	US-11-371-354-55428	Sequence 55428, A
c 39	69.8	18.4	2950	8	US-11-266-748A-24706	Sequence 24706, A
c 40	66.6	17.6	2227	10	US-11-414-896A-1	Sequence 1, Appli
c 41	66.6	17.6	2360	8	US-11-266-748A-57526	Sequence 57526, A
c 42	66.4	17.5	1000	8	US-11-266-748A-402012	Sequence 402012,
c 43	66.4	17.5	1000	8	US-11-266-748A-473058	Sequence 473058,
c 44	66.4	17.5	1575	7	US-11-371-354-65796	Sequence 65796, A
c 45	66.4	17.5	1676	6	US-10-196-749-203	Sequence 203, App

## ALIGNMENTS

## RESULT 1

US-10-540-310-3/c

; Sequence 3, Application US/10540310

; Publication No. US20060166212A1

; GENERAL INFORMATION: